



#5

1

SEQUENCE LISTING

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<110> CIHLAR, TOMAS

<120> NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER

<130> 240.1PCD

<140> 10/086,816

<141> 2002-02-28

<150> 09/330,245

<151> 1999-06-10

<150> 60/132,267

<151> 1999-05-03

<150> 60/088,864

<151> 1998-06-11

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<170> PatentIn Ver. 2.1

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ggactcagct cccgggaagc aacccagctg cggaggcaac ggcagtgtcg ctccctccagc 180

gaaggacagc aggcaaggcag acagacagag gtcctggac tggaaaggct cagccccag 240

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Met Ala Phe Asn Asp Leu Leu Gln Gln Val

1

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10

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Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu

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ccc ctg ctc ctg atg gct tct cac aac acc ctg cag aac ttc act gct 388
Pro Leu Leu Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr Ala

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gcc atc cct acc cac cac tgc cgc ccg cct gcc gat gcc aac ctc agc 436
Ala Ile Pro Thr His His Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser

45

50

55

aag aac ggg ggg ctg gag gtc tgg ctg ccc cgg gac agg cag ggg cag Lys Asn Gly Gly Leu Glu Val Trp Leu Pro Arg Asp Arg Gln Gly Gln	484
60 65 70	
cct gag tcc tgc ctc cgc ttc acc tcc ccg cag tgg gga ctg ccc ttt Pro Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe	532
75 80 85 90	
ctc aat ggc aca gaa gcc aat ggc aca ggg gcc aca gag ccc tgc acc Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr	580
95 100 105	
gat ggc tgg atc tat gac aac agc acc ttc cca tct acc atc gtg act Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile Val Thr	628
110 115 120	
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125 130 135	
tcc ttg tac atg gtg ggg gtg ctg ctc gga gcc atg gtg ttc ggc tac Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met Val Phe Gly Tyr	724
140 145 150	
ctt gca gac agg cta ggc cgc cgg aag gta ctc atc ttg aac tac ctg Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu	772
155 160 165 170	
cag aca gct gtg tca ggg acc tgc gca gcc ttc gca ccc aac ttc ccc Gln Thr Ala Val Ser Gly Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro	820
175 180 185	
atc tac tgc gcc ttc cgg ctc ctc tcg ggc atg gct ctg gct ggc atc Ile Tyr Cys Ala Phe Arg Leu Leu Ser Gly Met Ala Leu Ala Gly Ile	868
190 195 200	
tcc ctc aac tgc atg aca ctg aat gtg gag tgg atg ccc att cac aca Ser Leu Asn Cys Met Thr Leu Asn Val Glu Trp Met Pro Ile His Thr	916
205 210 215	
cgg gcc tgc gtg ggc acc ttg att ggc tat gtc tac agc ctg ggc cag Arg Ala Cys Val Gly Thr Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln	964
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235 240 245 250	
cag cta ctg gtc tct gcg cct ttt gcc ttc ttc atc tac tcc tgg Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp	1060
255 260 265	
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270 275 280	

ctc acc ctg agg gcc ctg cag aga gtc gcc cg ^g atc aat ggg aag cgg Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Arg 285 290 295	1156
gaa gaa gga gcc aaa ttg agt atg gag gta ctc cg ^g gcc agt ctg cag Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu Gln 300 305 310	1204
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cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg tgg Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu Trp 335 340 345	1300
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ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt cgc Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly Arg 380 385 390	1444
cg ^g cct gcc cag atg gct gca ctg ctg gca ggc atc tgc atc ctg Arg Pro Ala Gln Met Ala Ala Leu Leu Ala Gly Ile Cys Ile Leu 395 400 405 410	1492
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gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc ttc Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe 430 435 440	1588
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gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc tac Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr 475 480 485 490	1732
ggt gct gtt cct gtg gcc ggc agc gct gtc act gtc ctc ctg cca gag Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro Glu 495 500 505	1780

acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc agg 1828
 Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg
 510 515 520

aaa ggg aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc 1876
 Lys Gly Lys Gln Thr Arg Gln Gln Glu His Gln Lys Tyr Met Val
 525 530 535

cca ctg cag gcc tca gca caa gag aag aat gga ctc tgaggactga 1922
 Pro Leu Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu
 540 545 550

gaaggggcct tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca 1982
 caaggaggag gaagaggaaa tggtgaccca agtgtggggg ttgtggttca ggaaagcattc 2042
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Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His
 35 40 45

Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu
 50 55 60

Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg
 65 70 75 80

Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala
 85 90 95

Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp
 100 105 110

Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys
 115 120 125

Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly
 130 135 140

Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly
 145 150 155 160

Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly
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 Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg
 180 185 190
 Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr
 195 200 205
 Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr
 210 215 220
 Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val
 225 230 235 240
 Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala
 245 250 255
 Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala
 260 265 270
 Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu
 275 280 285
 Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu
 290 295 300
 Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys Glu Leu Thr Met Gly
 305 310 315 320
 Lys Gly Gln Ala Ser Ala Met Glu Leu Leu Arg Cys Pro Thr Leu Arg
 325 330 335
 His Leu Phe Leu Cys Leu Ser Met Leu Trp Phe Ala Thr Ser Phe Ala
 340 345 350
 Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly Phe Gly Val Ser Ile Tyr
 355 360 365
 Leu Ile Gln Val Ile Phe Gly Ala Val Asp Leu Pro Ala Lys Leu Val
 370 375 380
 Gly Phe Leu Val Ile Asn Ser Leu Gly Arg Arg Pro Ala Gln Met Ala
 385 390 395 400
 Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro
 405 410 415
 Gln Asp Gln Ser Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly
 420 425 430
 Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu
 435 440 445
 Tyr Pro Thr Met Ile Arg Gln Thr Gly Met Gly Ser Thr Met
 450 455 460

Ala Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu
 465 470 475 480

Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val Ala
 485 490 495

Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln Pro Leu
 500 505 510

Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Lys Gly Lys Gln Thr Arg
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Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu Gln Ala Ser Ala
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<212> DNA

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 consensus sequence

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<210> 6
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